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Remarks begin on page 8

## **Amendments to the Claims**

This listing of the claims will replace all prior versions, and listings, of claims in this application.

## **Listing of Claims**

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- 1. (currently amended) A method <u>for determining whether a of screening for</u> candidate agents <u>is</u> capable of modulating germline transcription, comprising:
  - a) adding a library of candidate agents to a plurality of cells;
  - b) preparing mRNA from said plurality of cells to form an mRNA mixture;
  - c) adding to said mixture at least a first RNAse protection probe (RPP) substantially complementary to a first germline mRNA from an immunoglobulin heavy chain gene locus to form a first hybridization complex between said first germline mRNA and said first RPP;
  - d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested; and
  - e) quantifying the amount of said first germline mRNA as compared to a cell in the absence of a candidate agent; and to thereby
  - $\frac{1}{2}$  identifying at least one  $\underline{a}$  candidate agent that alters the amount of said first germline mRNA.
  - 2. (original) A method according to claim 1, further comprising stimulating said cells to produce germline mRNA.
  - 3. (original) A method according to claim 1, wherein said RPP is labeled.
  - 4. (original) A method according to claim 3, wherein said label is a fluorescent label.
  - 5. (original) A method according to claim 3, wherein said label is a radioisotope.

6. (original) A method according to claim 1, wherein said germline mRNA is Ig alpha1.

- 7. (original) A method according to claim 1, wherein said germline mRNA is Ig alpha-2.
- 8. (original) A method according to claim 1, wherein said germline mRNA is Ig epsilon.
- 9. (original) A method according to claim 1, wherein said germline mRNA is Ig gamma-1.
- 10. (original) A method according to claim 1, wherein said germline mRNA is Ig gamma-2.
- 11. (original) A method according to claim 1, wherein said germline mRNA is Ig gamma-3.
- 12. (original) A method according to claim 1, wherein said germline mRNA is lg gamma-4.
- 13. (original) A method according to claim 1, wherein said RPP has a sequence selected from the group consisting of the sequences depicted in Figure 3.
- 14. (original) A method according to claim 1, wherein said RPP has a sequence selected from the group consisting of the sequences depicted in Figure 4.
- 15. (cancelled)
- 16. (cancelled)

17. (Currently amended) A method according to claim 1, further comprising:

- a) adding to said mixture at least a second RNAse protection probe (RPP) substantially complementary to a second germline mRNA to form a second hybridization complex between said second germline mRNA and said second RPP;
- b) quantifying the amount of said second germline mRNA as compared to a cell in the absence of a candidate agent; and to thereby
  - e) identifying at least one a candidate agent that alters the amount of said first germline mRNA but not said second germline mRNA.
- 18. (Currently amended) A method according to claim 1, wherein said <del>library</del> comprises candidate agent is a small molecules.
- 19. (Currently amended) A method according to claim 1, wherein said <del>library</del> comprises candidate agent is a peptides.
- 20. (Currently amended) A method according to claim 19, wherein said peptides are is a random peptides.
- 21. (Currently amended) A method according to claim 19, wherein said peptides are is a partially random peptides.
- 22. (Currently amended) A method according to claim 19, wherein said adding is done using <u>a</u> retroviruses encoding said peptides.
- 23. (Currently amended) A method according to claim 19 wherein said adding is done using <u>a</u> retroviruses comprising sequence derived from a cDNA library.
- 24. (withdrawn) A method of quantifying the amount of a plurality of germline constructs comprising:

a) preparing mRNA from said plurality of cells to form an mRNA mixture;

- c) adding at least three RNAse protection probes (RPPs) selected from the group consisting of the sequences depicted in Figures 3 and 4;
- d) adding an RNAse protection enzyme (RPE) to said mixture, such that mRNA that is not protected is digested;
- e) quantifying the amount of said germline mRNA.
- 25. (withdrawn) A kit for quantifying the amount of germline mRNA in a sample, comprising
  - a) at least one RNAse protection probe (RPP) comprising a nucleic acid sequence selected from the group consisting of the nucleic acid sequences of the Igα1, Igα2, Ig-epsilon, Ig gamma-1, Ig gamma-2, Ig gamma-3 and Ig gamma-4 RPPs set forth in Figures 3 and 4; and
  - an RNAse protection enzyme (RPE);
    and optionally comprising at least one RNAse protection probe (RPP) which is substantially complementary to a transcript of a housekeeping gene.
- 26. (withdrawn) A kit according to claim 25, wherein all RNAse protection probes are labeled.
- 27. (New) The method of claim 1, wherein said first RNAse protection probe (RPP) and said first germline mRNA contain less than 5 base mismatches.
- 28. (New) A method according to claim 6, wherein said RPP comprises the sequence set forth as SEQ ID NO:7.
- 29. (New) A method according to claim 7, wherein said RPP comprises the sequence set forth as SEQ ID NO:1 or 8.
- 30. (New) A method according to claim 8, wherein said RPP comprises the sequence set forth as SEQ ID NO:2 or 9.

31. (New) A method according to claim 9, wherein said RPP comprises the sequence set forth as SEQ ID NO:3 or 10.

- 32. (New) A method according to claim 10, wherein said RPP comprises the sequence set forth as SEQ ID NO:4 or 11.
- 33. (New) A method according to claim 11, wherein said RPP comprises the sequence set forth as SEQ ID NO:5 or 12.
- 34.(New) A method according to claim 12, wherein said RPP comprises the sequence set forth as SEQ ID NO:6 or 13.